

	1	11 15
ζ	QSFGLLDPK	LCYLLDG--
	369	
CD4: ζ	--PTWSTPVHADPK	LCYLLDG--
<hr/>		
	1	
γ	LGEPQ	LCYILDA--
	369	
CD4: γ	--PTWSTPVHADPQ	LCYILDA--

Fig. 1a

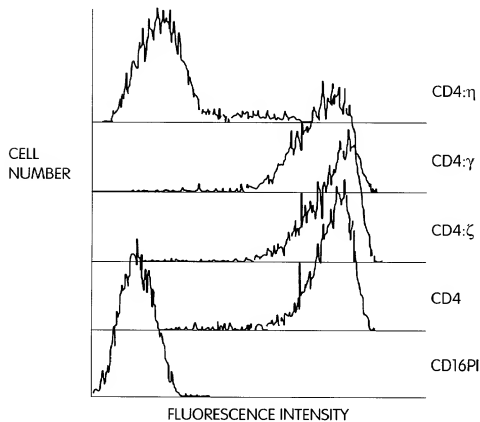


Fig. 1b

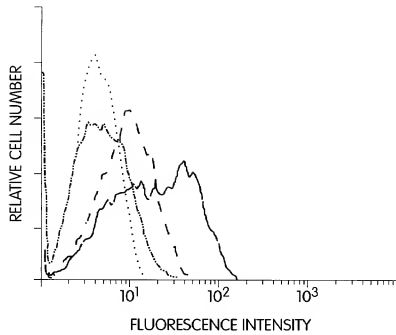


Fig. 2

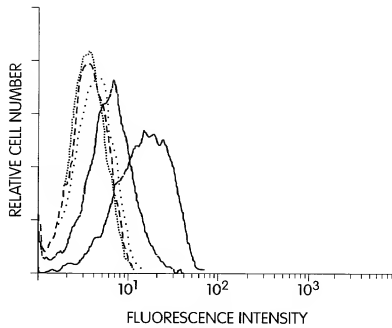


Fig. 3

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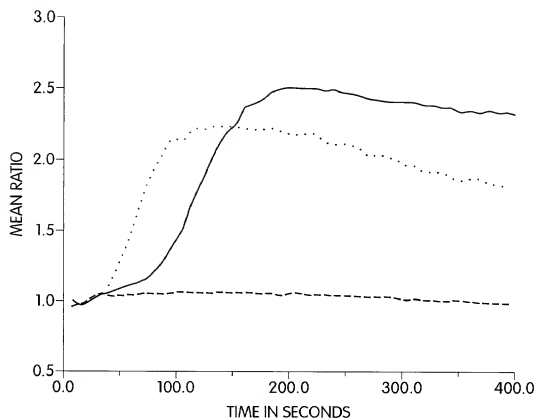


Fig. 4a

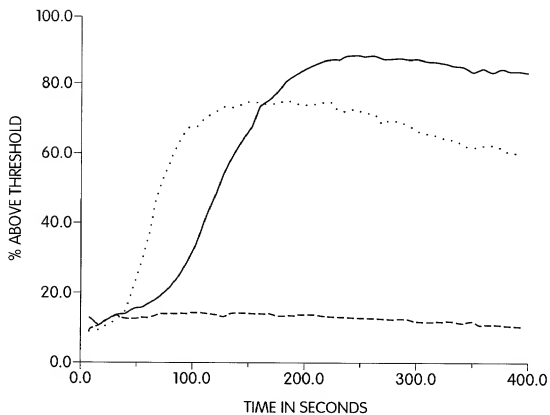


Fig. 4b

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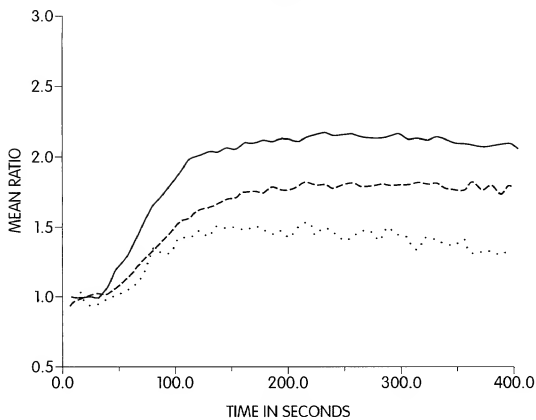


Fig. 4c

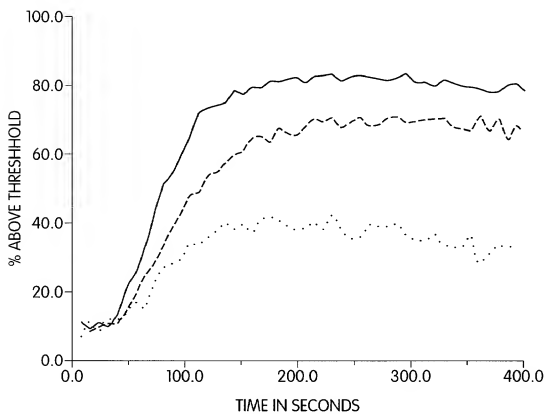


Fig. 4d

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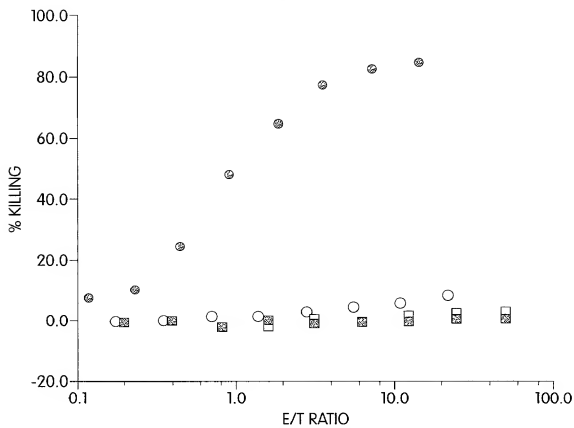


Fig. 5a

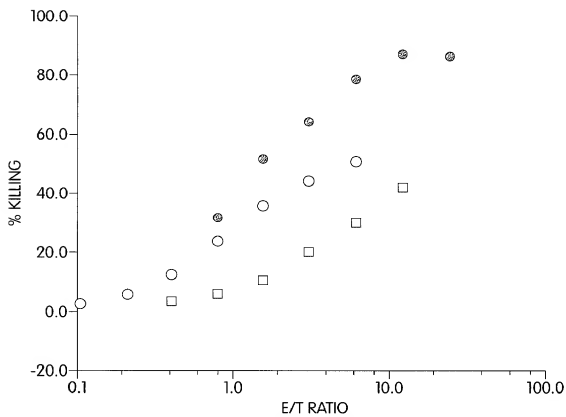


Fig. 5b

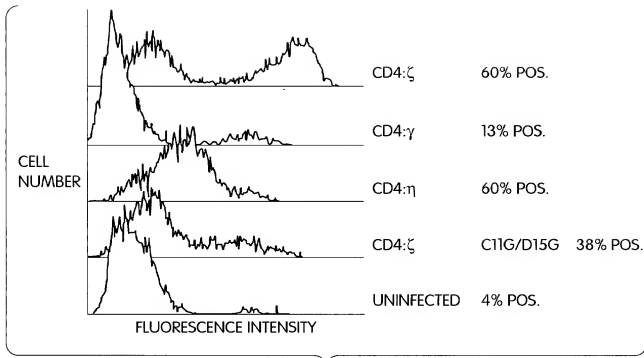


Fig. 5c

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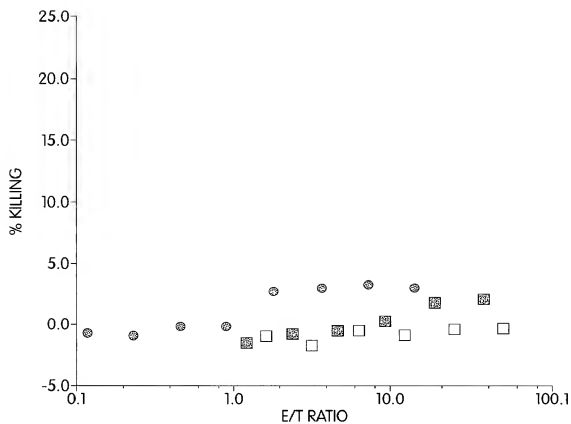


Fig. 6a

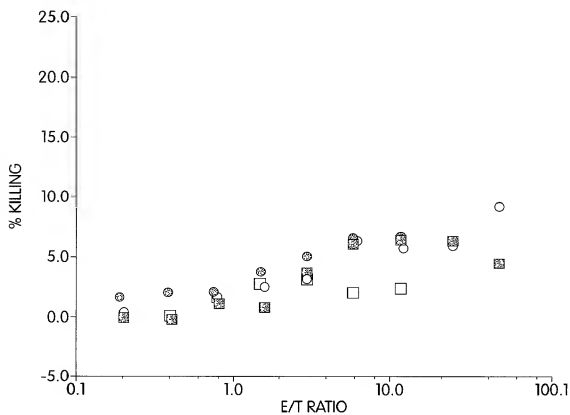


Fig. 6b

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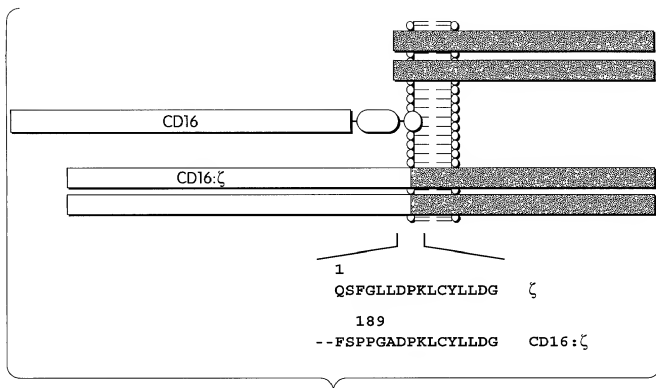


Fig. 7a

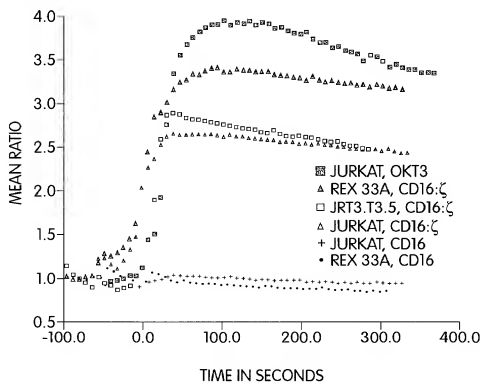


Fig. 7b

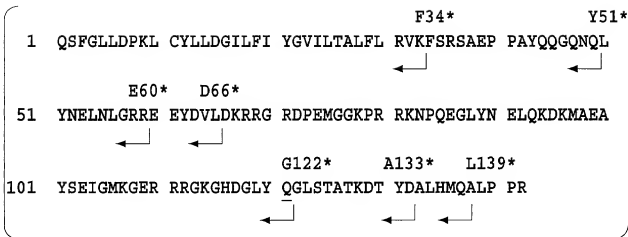


Fig. 8a

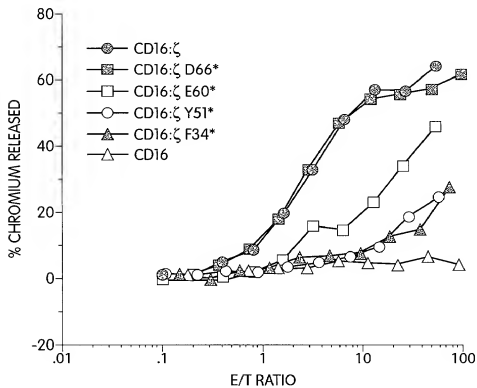


Fig. 8b

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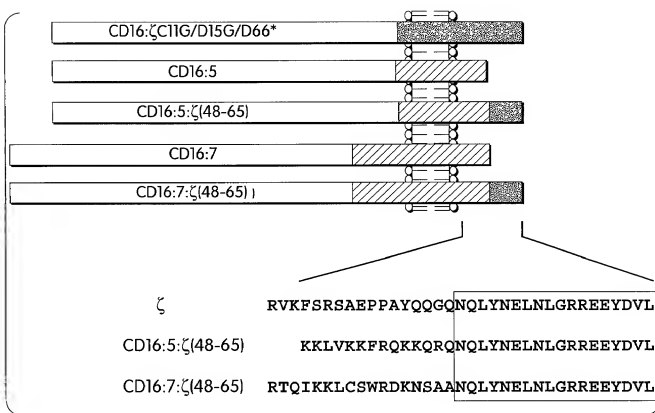


Fig. 9a

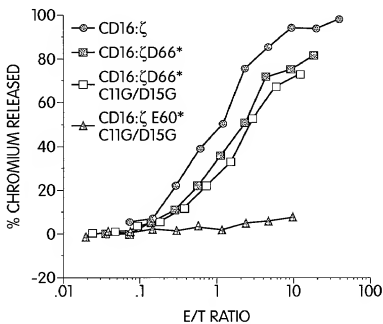


Fig. 9b

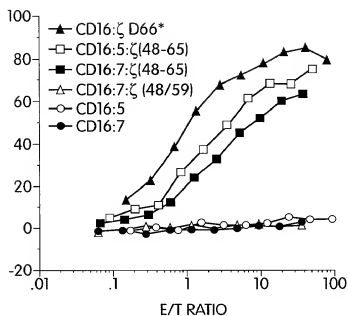


Fig. 9c

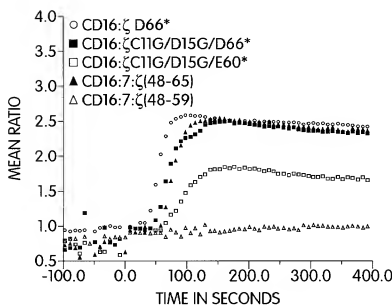


Fig. 9d

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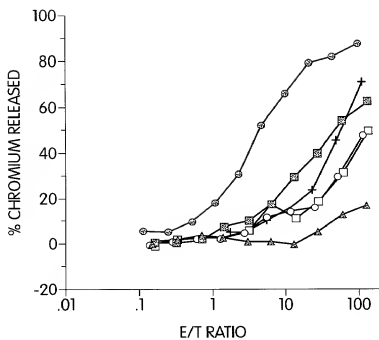


Fig. 10a

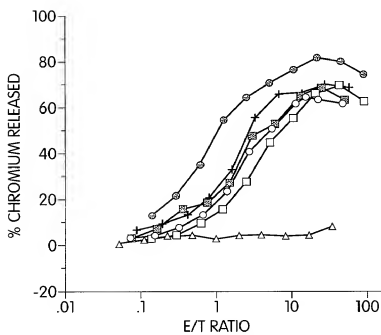


Fig. 10b

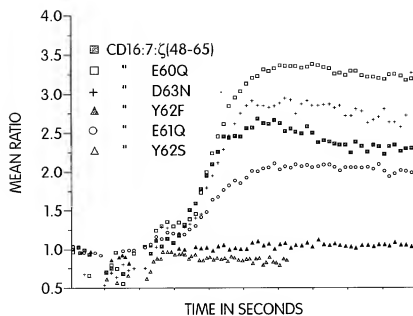


Fig. 10c

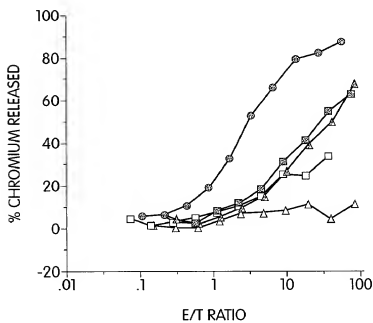


Fig. 10d

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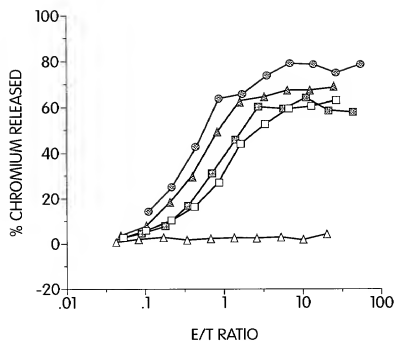


Fig. 10e

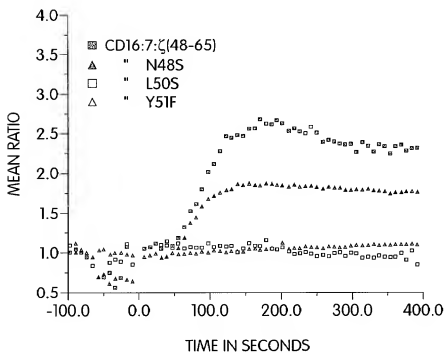


Fig. 10f

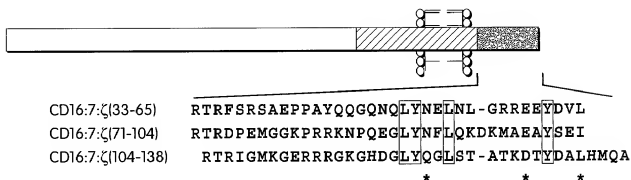


Fig. 11a

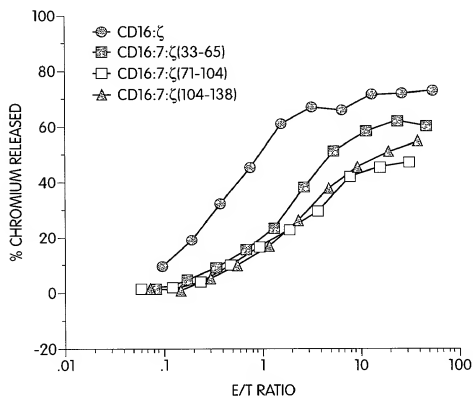


Fig. 11b

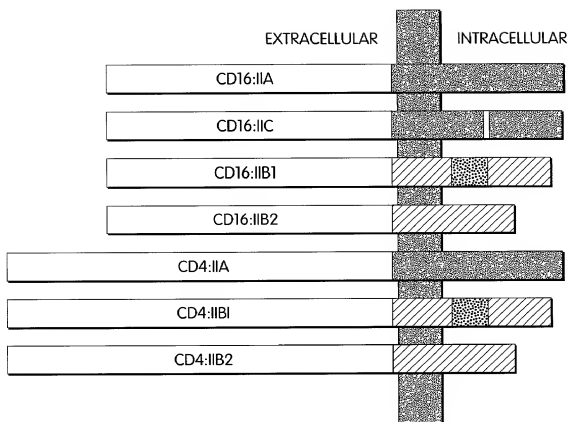


Fig. 12

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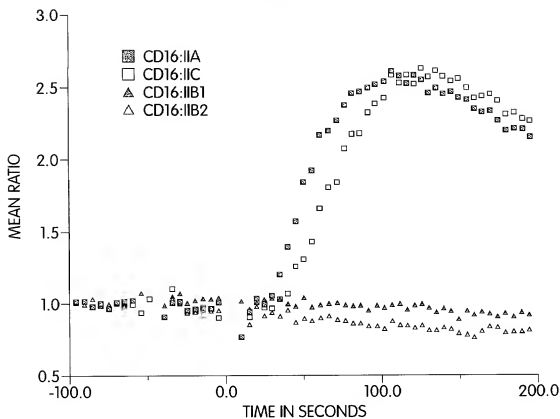


Fig. 13a

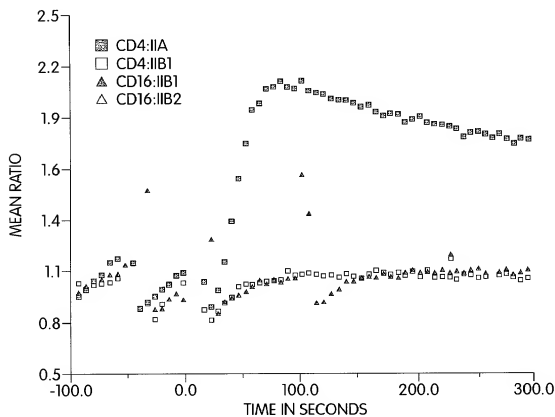


Fig. 13b

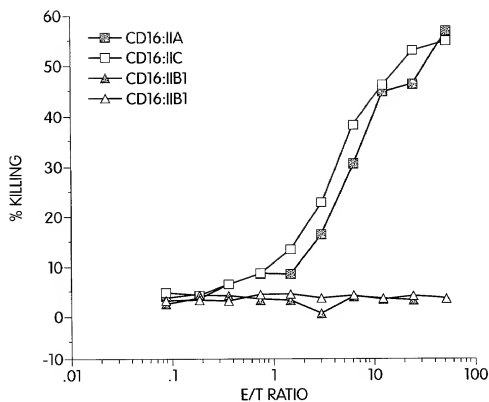


Fig. 14a

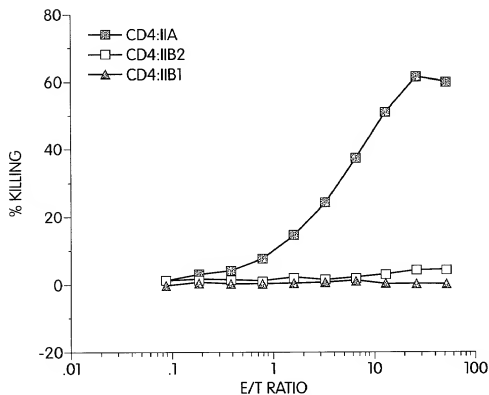


Fig. 14b

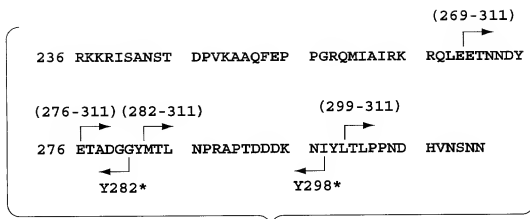


Fig. 15a

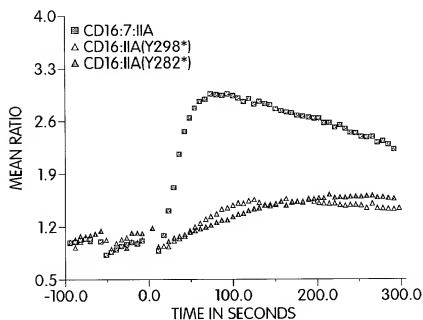


Fig. 15b

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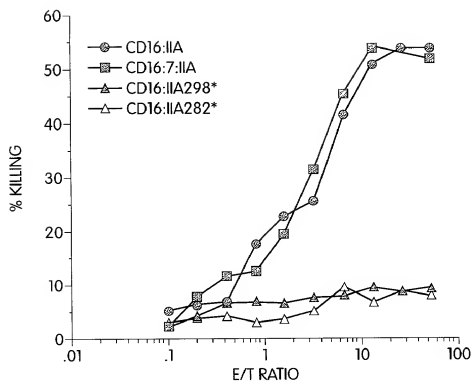


Fig. 15c

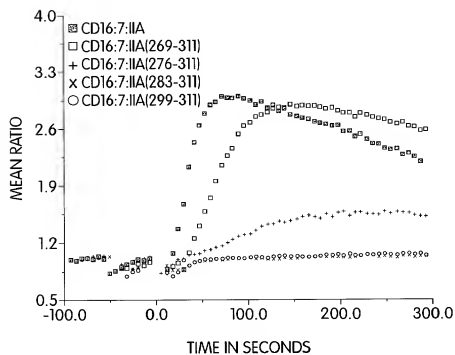


Fig. 15d

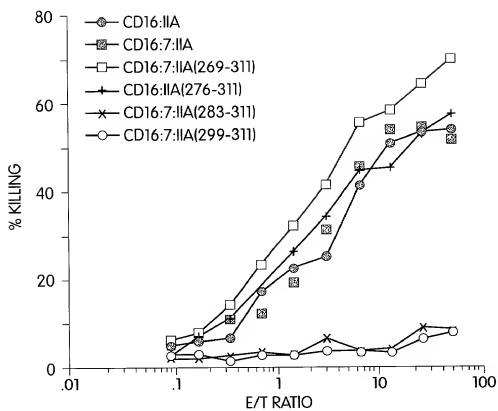


Fig. 15e

(Seq. ID No: 24)

1	MEHSTFLSGL	VLATLLSQVS	PFKIPIEELE	DRVFNVCNTS	ITWVEGTVGT
51	LLSDITRLDL	GKRILDPGRI	YRCNGTDIYK	DKESTVQVHY	RMCQSCVEID
101	PATVAGIIVT	DVIATLLAL	GVFCFAGHET	<u>GRLSGAADTQ</u>	<u>ALLRNDQVYQ</u>
151	<u>PLRDRDDAQY</u>	<u>SHLGGNWARN</u>	<u>K*</u>		

Fig. 16

(Seq ID NO: 25)

1	MEQQKGLAVL	ILAIILLQGT	LAQSIKGNHL	VKVYDYQEDG	SVLLTCDAAE
51	KNITWFKDGK	MIGFLTEDKK	KWNLGSNAKD	PRGMYQCKGS	QNKSKPLQVY
101	YRMCQNCIEL	NAATISGFLF	AEIVSIFVLA	VGVIYFIAGQD	<u>GVRQSRASDK</u>
151	<u>QTLLPNDQLY</u>	<u>QPLKDREDDQ</u>	<u>YSHLQGNQLR</u>	<u>RN*</u>	

Fig. 17

(Seq ID No: 26)

1	MPGGLEALRA	LPLLLFLSYA	CLGPGCQALR	VEGGPPSLTV	NLGEEARLTC
51	ENNGRNPNT	WWFSLQSNIT	WPPVPLGPGQ	GTTGQLFFPE	VNKNTGACTG
101	CQVIENNILK	RSCGTYLVR	NPVPRPFLDM	GEGTKNRIT	<u>AEGIILLFCA</u>
151	VVPGTLLLFR	<u>KRWQNEKFGV</u>	DMPDDYEDEN	LYEGLNLDDC	SMYEDISRGL
201	<u>QGTYQDVGNL</u>	<u>HIGDAQLEKP</u>	<u>*</u>		

Fig. 18

(Seq ID No: 27)

1	MATLVLSSMP	CHWLLFLLLL	FSGEPVPAMT	SSDPLPLNFQG	SPCSQIWQHP
51	RFAAKKRSSM	VKFHCYTNHS	GALTWFRKRG	SQQPQELVSE	EGRIQVTQNG
101	SVYTLTIQNI	QYEDNGIYFC	KQKCDSANHN	VTDSCTELL	VLGFSTLDQL
151	KRRNTLKDGI	ILIQTLIIIL	FIIVPIFLLL	<u>DKDGGKAGME</u>	<u>EDHTYEGLNI</u>
201	<u>DQTATYEDIV</u>	<u>TLRTGEVKWS</u>	<u>VGEHPGQE*</u>		

Fig. 19

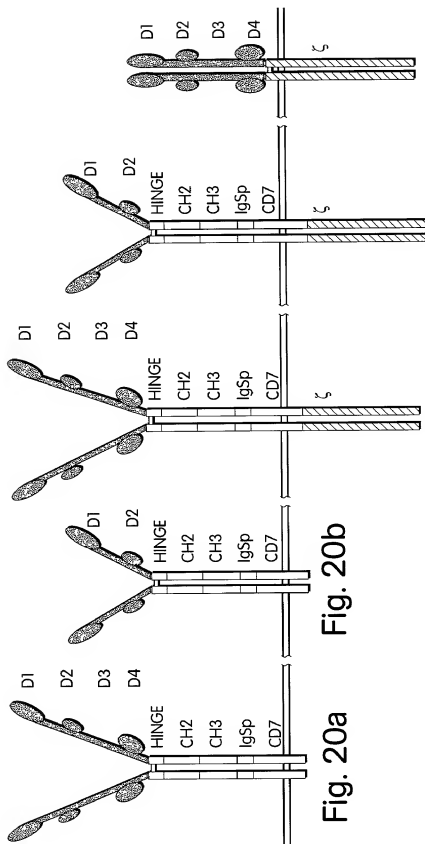


Fig. 20a Fig. 20b

Fig. 20c Fig. 20d Fig. 20e

BamHI/BstYI

Bgl2/BstYI

G GAT CCC AAG GCC AGG CTA AAG CCG AAG CCG CGA AGG CCG AGG CTA AGG CCG AAG CAG ATC TG
D P K A E A K A E A K A E A D L

Fig. 28

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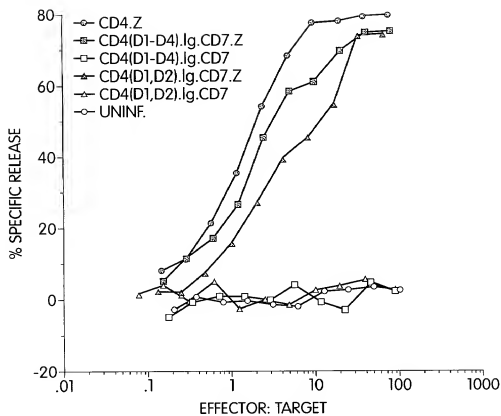


Fig. 21

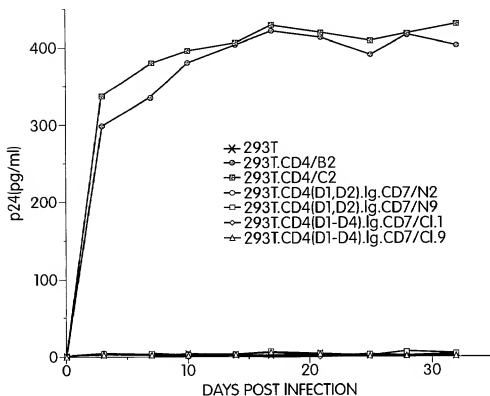


Fig. 22

D1 - D4 of CD4

Nucleic Acid Sequence

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GCCTGTTTGA GAAGCAGCGG GCAAGAAAGA CGCAAGCCCA GAGGCCCTGC 51
CATTCTGTGT GGCTCAGGTC CCTACTGGCT CAGGCCCTCTG CCTCCTCTGG 101
CAAGGCCACA ATGAACCGGG GAGTCCCTTT TAGGCACCTTG CTTCTGGTGC 151
TGCAACTGGC GCTCCTCCCA GCAGCCACTC AGGGAAACAA AGTGGTGCTG 201
GGCAAAAAAG GGGATACAGT GGAAGTACC TGTACAGCTT CCCAGAAGAA 251
GAGCATACAA TTCCACTGGA AAAACTCCAA CCAGATAAAG ATTCTGGGGA 301
ATCAGGGCTC CTCTTAACT AAAGGTCCAT CCAAGCTGAA TGATCGCGCT 351
GACTCAAGAA GAAGCCTTTG GGACCAAGGA AACTTCCCCC TGATCATCAA 401
GAATCTTAAG ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGACC 451
AGAAGGAGGA GGTGCAATTG CTAGTGTTTG GATTGACTGC CAACTCTGAC 501
ACCCACCTGC TTCAGGGGCA GAGCTTGACC CTGACCTTGG AGAGCCCCC 551
TGGTAGTAGC CCCTCAGTGC AATGTAGGAG TCCAAGGGTG AAAACATAC 601
AGGGGGGGAA GACCTCTCC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC 651
ACCTGGACAT GCACTGTCTT GCAGAACCAG AAGAAGGTGG AGTTCAAAAT 701
AGACATCGTG GTGCTAGCTT TCCAGAAGGC CTCAGCATA GTCTATAAGA 751
AAGAGGGGGA ACAGGTGGAG TTCTCCTTCC CACTCGCCTT TACAGTTGAA 801
AAGCTGACGG GCAGTGGCGA GCTGTGGTGG CAGGCGGAGA GGGCTTCTCT 851
CTCCAAGTCT TGGATCACCT TTGACCTGAA GAACAAGGAA GTGTCTGTAA 901
AACGGGTTAC CCAGGACCCT AAGCTCCAGA TGGGCAAGAA GCTCCCGCTC 951
CACCTCACCC TGCCCCAGGC CTTGCCTCAG TATGCTGGCT CTGGAACCT 1001
CACCTGGGCC CTTGAAGCGA AAACAGGAAA GTTGACATCAG GAAGTGAACC 1051
TGGTGGTGAT GAGAGCCACT CAGCTCCAGA AAAATTGAC CTGTGAGGTG 1101
TGGGGACCCA CCTCCCCTAA GCTGATGCTG AGCTTGAAAC TGGAGAACAA 1151
GGAGGCAAAAG GTCTCGAAGC GGGAGAAGCC GGTGTGGGTG CTGAACCTCTG 1201
AGGCGGGGAT GTGCGAGTGT CTGCTGAGTG ACTCGGGACA GTGCTGTGCTG 1251
GAATCCAACA TCAAGGTTCT GCCCACATGG TCCACCCCGG TGCACGCGGA 1301
TCCC (SEQ ID NO: 28)

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Amino Acid Sequence

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MNRGVPPFRL LVLQLALLP AATQGNKVVL GKKGDTVELT CTASQKKSIQ 51
FHWKNSQIK ILGNQGSFLT KGPSKLNDRS DSRRSLWDQG NFPLIKNLK 101
IEDSDTYICE VEDQKEEVQL LVFGLTANS DTHLLQGQSLT LTLESPPGSS 151
PSVQCRSPRG KNIQGGKTL S VSQLELQDSG TWTCTVLQNG KKEVEFKIDIV 201
VLAFQKASSI VYKKEGEQVE FSFPLAFTVE KLTGSSELWW QAERASSSKS 251
WITFDLKNKE VSVKRVTDQP KLQMGKYLPL HLTLPQALPQ YAGSGNLTLA 301
LEAKTKLHQH EVNLVVMRAT QLQKNLTCEV WGPTSPKMLL SKLENKEAK 351
VSKREKPVVW LNPEAGMWQC LLSDSGQVLL ESNIKVLPTW STPVHADP
(SEQ ID NO: 29)

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D1 - D2 of CD4

Nucleic Acid Sequence

GCCTGTTTGA GAAGCAGCGG GCAAGAAAGA CGCAAGCCCA GAGGCCCTGC 51
 CATTTCTGTG GGCTCAGGTC CCTACTGGCT CAGGCCCTCG CCTCCCTCGG 101
 CAAGGCCACA ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC 151
 TGCAACTGGC GCTCCTCCCA GCAGCCACTC AGGGAAACAA AGTGGTGTCTG 201
 GGCAAAAAAG GGGATACAGT GGAAGTGACC TGTACAGCTT CCCAGAAGAA 251
 GAGCATACAA TTCCACTGGA AAAACTCCAA CCAGATAAAG ATTCTGGGAA 301
 ATCAGGGCTC CTTCTTAACT AAAGGTCCAT CCAAGCTGAA TGATCGCGCT 351
 GACTCAAGAA GAAGCCTTTG GGACCAAGGA AACTTCCCCC TGATCATCAA 401
 GAATCTTAAG ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGACC 451
 AGAAGGAGGA GGTGCAATTG CTAGTGTTTC GATTGACTGC CAACTCTGAC 501
 ACCCACCTGC TTCAGGGGCA GAGCCTGACC CTGACCTTGG AGAGCCCCC 551
 TGGTAGTAGC CCCTCAGTGC AATGTAGGAG TCCAAGGGGT AAAAACATAC 601
 AGGGGGGGAA GACCTCTCC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC 651
 ACCTGGACAT GCACTGTCTT GCAGAACCAG AAGAAGGTGG AGTTCAAAAT 701
 AGACATCGTG GTGCTAGCT (SEQ ID NO: 30)

Amino Acid Sequence

MNRGVPPRHL LLVLQLALLP AATQGNKVVL GKKGDTVELT CTASQKKSIIQ 51
 FHWKNSNQIK ILGNQGSFLT KGPSKLNDRD DSRRSLWDQG NFPLIIKNLK 101
 IEDSDTYICE VEDQKEEVQL LVFGLTANS DTHLLQGQSLT LTLESPPGSS 151
 PSVQCRSPRG KNIQGGKTL S VSQLELQDSG TWTCTVLQNO KKVEFKIDIV 201
 VLA (SEQ ID NO: 31)

Fig. 24

Hinge, CH2, and CH3 Domains of Human IgG1

Nucleic Acid Sequence

```

GCTAGCAGAG CCCAAATCTT GTGACAAAAC TCACACATGC CCACCGTGCC 51
CAGCACCTGA ACTCCTGGGG GGACCGTCAG TCTTCCTCTT CCCCCCAAAA 101
CCCAAGGACA CCTCATGAT CTCCCGGACC CCTGAGGTCA CATGCGTGGT 151
GGTGGACGTG AGCCACGAAG ACCCTGAGGT CAAGTTCAAC TGGTACGTGG 201
ACGGCGTGGA GGTGCATAAT GCCAAGACAA AGCCGCGGGA GGAGCAGTAC 251
AACAGCACGT ACCGGGTGGT CAGCGTCCTC ACCGTCTGTC ACCAGGACTG 301
GCTGAATGGC AAGGAGTACA AGTGCAAGGT CTCCAACAAA GCCCTCCCAG 351
CCCCCATCGA GAAAACCATC TCCAAAGCCA AAGGGCAGCC CCGAGAACCA 401
CAGGTGTACA CCTGCCCCC ATCCCGGGAT GAGCTGACCA AGAACCAGGT 451
CAGCCTGACC TGCTTGCTCA AAGGCTTCTA TCCAGCGCAC ATCGCCGTGG 501
AGTGGGAGAG CAATGGGCAG CCGGAGAACA ACTACAAGAC CACGCTCCCC 551
GTGCTGGACT CCGACGGCTC CTTCTTCCTC TACAGCAAGC TCACCGTGGA 601
CAAGAGCAGG TGGCAGCAGG GGAACGTCTT CTCATGCTCC GTGATGCATG 651
AGGCTCTGCA CAACCACTAC ACGCAGAAGA GCCTCTCCCT GTCTCCGGGG 701
CTGCAACTGG ACGAGACCTG TGCTGAGGCC CAGGACGGGG AGCTGGACGG 751
GCTCTGGACG ACGGATCC (SEQ ID NO: 32)

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Amino Acid Sequence

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EPKSCDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD 51
VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN 101
GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR DELTKNQVSL 151
TCLVKGFPYS DIAVEWESNG QPENNYKTP PVLDSGDSFF LYSKLTVDKS 201
RWQQGNVFSC SVMHEALHNNH YTKSLSLSP GLQLDETCAE AQDGLDGLW 251
TTDP (SEQ ID NO: 33)

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Fig. 25

CD7 Transmembrane Domain

Nucleic Acid Sequence

CCAAGGGCCT CTGCCCTCCC TGCCCCACCG ACAGGCTCCG CCCTCCCTGA 51
 CCCGCAGACA GCCTCTGCCC TCCCTGACCC GCCAGCAGCC TCTGCCCTCC 101
 CTGCGGCCCT GCGCGTGATC TCCTTCCTCC TCGGGCTGGG CCTGGGGGTG 151
 GCGTGTGTGC TGGCGAGGAC GCGT (SEQ ID NO: 34)

Amino Acid Sequence

PRASALPAPP TGSALPDPQT ASALPDPPAA SALPAALAVI SFLLGLGLGV 51
 ACVLARTR (SEQ. ID NO: 35)

Fig. 26

Zeta Intracellular Domain

Nucleic Acid Sequence

ACGCGTTTCA GCAGGAGCGC AGAGCCCCC GCGTACCAGC AGGGCCAGAA 51
 CCAGCTCTAT AACGAGCTCA ATCTAGGACG AAGAGAGGAG TACGATGTTT 101
 TGGACAAGAG ACGTGGCCGG GACCCTGAGA TGGGGGGAAA GCCGAGAAGG 151
 AAGAACCCTC AGGAAGGCCT GTACAATGAA CTGCAGAAAG ATAAGATGGC 201
 GGAGGCCCTAC AGTGAGATTG GGATGAAAGG CGAGCGCCCG AGGGGCAAGG 251
 GGCACGATGG CCTTTACCAG GGTCTCAGTA CAGCCACCAA GGACACCTAC 301
 GACGCCCTTC ACATGCAGGC CCTGCCCCCT CGCTAAAGCG GCCGC
 (SEQ ID NO: 36)

Amino Acid Sequence

TRFSRSAEPP AYQQGQNQLY NELNLGRREE YDVLDKRRGR DPEMGGKPRR 51
 KNPQEGLYNE LQKDKMAEAY SEIGMYGERR RGKGHDGLYO GLSTATKDTY 101
 DALHMQUALPP R (SEQ ID NO: 37)

Fig. 27